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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/817,198	03/27/2001	Jane Ye	CL001188	9081

7590 05/11/2004
CELERA GENOMICS CORPORATION
45 West Gude Dr. C2-4#20
Rockville, MD 20850

EXAMINER

RAWLINGS, STEPHEN L

ART UNIT	PAPER NUMBER
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1642

17

DATE MAILED: 05/11/2004

Please find below and/or attached an Office communication concerning this application or proceeding.



UNITED STATES DEPARTMENT OF COMMERCE

U.S. Patent and Trademark Office

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Alexandria, Virginia 22313-1450

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER

ART UNIT	PAPER
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17

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

NOTIFICATION OF SUSPENSION

All claims are presently allowable. However, a reference relevant to the examination of this application may soon become available. Therefore, *ex parte* prosecution is SUSPENDED FOR A PERIOD OF SIX (6) MONTHS from the date of this letter. Upon expiration of the period of suspension, applicant should make an inquiry as to the status of the application.


Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stephen L. Rawlings, Ph.D. whose telephone number is (571) 272-0836. The examiner can normally be reached on Monday-Friday, 8:30AM-5:00PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Yvonne (Bonnie) Eyler, Ph.D. can be reached on (571) 272-0871. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Stephen L. Rawlings, Ph.D.
Examiner
Art Unit 1642

slr
April 7, 2004


YVONNE EYLER, PH.D.
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Attachment: Form PTO-1449, Paper No. 16.



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Jane YE et al.

Art Unit: 1642

Serial No.: 09/817,198

Examiner: S. Rawlings

Filed: March 27, 2001

Atty. Docket: CL001188

For: ISOLATED HUMAN RAS-LIKE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN RAS-LIKE
PROTEINS, AND USES THEREOF

RECEIVED

AUG 18 2003

TECH CENTER 1600/2900

**Statement Regarding Duty to Disclose Information Material To Patentability Under
37 CFR 1.56 (a) and (b)**

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Applicants hereby notify the US Patent and Trademark Office of the documents listed on the attached PTO Form SB/08A, which may be deemed relevant to the patentability of the claims of the above application. One copy of each of the listed documents is submitted herewith. The submission of the listed documents is not intended as an admission that any such document constitutes prior art against the claims of the present application.

Please charge the fee set forth in §1.17(p) to deposit account number 50-0970. Furthermore, the Office is authorized to charge any other necessary fees related to the processing of this application to Deposit Account No. 50-0970.

Respectfully submitted,
CELERA GENOMICS

Date: August 15, 2003

By: Justin D. Karjala
Justin D. Karjala, Reg No. 43,704

Celera Genomics Corporation
45 West Gude Drive, C2-4#21
Rockville, MD 20850
Tel: 240-453-3812
Fax: 240-453-3084

Patent Screen Results

Your Fasta Input (protein sequence):

>CL001188, SEQ ID NO:2, July 22, 2003

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1 MAKQYDVLFR LLLIGDSGVG KTCLLCRFTD NEFHSSHIST IGVDFKMKTI
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151 SACTNLNIKE SFTRLTELVL QAHRKELEGL RMRASNELAL AELEEEEGKP
201 EGPANSSKTC WC

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BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= CL001188, SEQ ID NO:2, July 22, 2003
(212 letters)

Database: /work/eda/blast/public/FastAlert_P.fasta
261,406 sequences; 38,879,213 total letters

Sequences producing significant alignments:	Score (bits)	E Value
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 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
 Sbjct: 27 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 86

Query: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120
 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG
 Sbjct: 87 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 146

Query: 121 NKADEEQKRQVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 180
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Query: 181 RMRASNELALAELEEEEGKPEGPANSSKTCWC 212
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Database: /work/eda/blast/public/FastAlert_P.fasta
Posted date: Mar 1, 2003 1:40 PM
Number of letters in database: 38,879,213
Number of sequences in database: 261,406

Lambda	K	H
0.317	0.134	0.389

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 15413235
Number of Sequences: 261406
Number of extensions: 575941
Number of successful extensions: 2573
Number of sequences better than 1.0e-08: 117
Number of HSP's better than 0.0 without gapping: 74
Number of HSP's successfully gapped in prelim test: 43
Number of HSP's that attempted gapping in prelim test: 2415
Number of HSP's gapped (non-prelim): 118
length of query: 212
length of database: 38,879,213
effective HSP length: 51
effective length of query: 161
effective length of database: 25,547,507
effective search space: 4113148627
effective search space used: 4113148627
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (21.7 bits)

S2: 139 (58.6 bits)

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= CL001188, SEQ ID NO:2, July 22, 2003
(212 letters)

Database: /work/eda3/blast/public/geneseqp_all.fasta
952,616 sequences; 143,563,330 total letters

Sequences producing significant alignments:	Score (bits)	E Value
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CRA 67000131173720 /dataset=GENESEQ /org=Homo sapiens /taxon=96...	214	3e-55
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CRA 335001100263522	/dataset=GENESEQ /org=Homo sapiens /taxon=9...	86	2e-16
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Score = 434 bits (1105), Expect = e-121
Identities = 212/212 (100%), Positives = 212/212 (100%)

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MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
Sbjct: 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60

Query: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120
IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG
Sbjct: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120

Query: 121 NKADEEQKRQVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 180
NKADEEQKRQVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL
Sbjct: 121 NKADEEQKRQVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 180

Query: 181 RMRASNELALAELEEEEGKPEGPANSSKTCWC 212
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/def=Novel signal transduction pathway protein, Seq ID
701 /patent=WO200154733-A1 /pat_section=Claim
Length = 401

Score = 434 bits (1105), Expect = e-121
Identities = 212/212 (100%), Positives = 212/212 (100%)

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MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
Sbjct: 27 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 86

Query: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120
IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG
Sbjct: 87 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 146

Query: 121 NKADEEQKRQVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 180
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Sbjct: 147 NKADEEQKRQVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 206

Query: 181 RMRASNELALAELEEEEGKPEGPANSSKTCWC 212
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Length = 212

Score = 434 bits (1105), Expect = e-121
Identities = 212/212 (100%), Positives = 212/212 (100%)

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 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKKTIEVDGIKVRIG
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Query: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120
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Query: 121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 180
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Query: 181 RMRASNELALAELEEEEGKPEGPANSSKTCWC 212
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 NO:2736 /patent=WO200058473-A2 /pat_section=Claim
 Length = 218

Score = 428 bits (1088), Expect = e-119
 Identities = 212/218 (97%), Positives = 212/218 (97%), Gaps = 6/218 (2%)

Query: 1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKKTIEVDGIKVRIG 60
 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKKTIEVDGIKVRIG
 Sbjct: 1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKKTIEVDGIKVRIG 60

Query: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120
 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG
 Sbjct: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120

Query: 121 NKADEEQKRQVGREQGQ-----QLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHR 174
 NKADEEQKRQVGREQGQ QLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHR
 Sbjct: 121 NKADEEQKRQVGREQGQKCPSLQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHR 180

Query: 175 KELEGLRMRASNELALAELEEEEGKPEGPANSSKTCWC 212
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 /def=Novel signal transduction pathway protein, Seq ID
 1120 /patent=WO200154733-A1 /pat_section=Claim
 Length = 188

Score = 328 bits (832), Expect = 2e-89
 Identities = 160/164 (97%), Positives = 160/164 (97%)

Query: 1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKKTIEVDGIKVRIG 60
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Sbjct: 24 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 83

Query: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120
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Sbjct: 84 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQXILIG 143

Query: 121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTR 164
 NKADEEQ RQVGREQGQ LA EYGMDFYETSACTNLNIKESFTR

Sbjct: 144 NKADEEQXRQVGREQGQXLAXEYGMDFYETSACTNLNIKESFTR 187

Database: /work/eda3/blast/public/geneseqp_all.fasta
 Posted date: Mar 2, 2003 3:26 AM
 Number of letters in database: 143,563,330
 Number of sequences in database: 952,616

Lambda	K	H
0.317	0.134	0.389

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 57070426
 Number of Sequences: 952616
 Number of extensions: 2081050
 Number of successful extensions: 9986
 Number of sequences better than 1.0e-08: 869
 Number of HSP's better than 0.0 without gapping: 504
 Number of HSP's successfully gapped in prelim test: 365
 Number of HSP's that attempted gapping in prelim test: 8851
 Number of HSP's gapped (non-prelim): 881
 length of query: 212
 length of database: 143,563,330
 effective HSP length: 54
 effective length of query: 158
 effective length of database: 92,122,066
 effective search space: 14555286428
 effective search space used: 14555286428
 T: 11
 A: 40
 X1: 16 (7.3 bits)
 X2: 38 (14.8 bits)
 X3: 64 (24.9 bits)
 S1: 41 (21.7 bits)
 S2: 144 (60.5 bits)

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= CL001188, SEQ ID NO:2, July 22, 2003
(212 letters)

Database: /work/eda/blast/public/pataa.fasta
119,338 sequences; 19,610,776 total letters

Searching.....done

Sequences producing significant alignments:							Score (bits)	E Value
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CRA 225000041421315	/altid=gi 5987941	/def=gb AAE17106.1	Seque...	209	2e-54			
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CRA 225000041408175	/altid=gi 5987951	/def=gb AAE17116.1	Seque...	196	1e-50			
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CRA 225000041399569	/altid=gi 5987936	/def=gb AAE17101.1	Seque...	133	2e-31			
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CRA 225000073419025	/altid=gi 29890315	/def=emb CAD88939.1	unn...	106	2e-23			
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Length = 212

Score = 434 bits (1105), Expect = e-122
Identities = 212/212 (100%), Positives = 212/212 (100%)

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MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
Sbjct: 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60

Query: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120
IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG
Sbjct: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWSDVDEYAPEGVQKILIG 120

Query: 121 NKADEEQKRQVGREQQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 180
NKADEEQKRQVGREQQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL
Sbjct: 121 NKADEEQKRQVGREQQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 180

Query: 181 RMRASNELALAELEEEEGKPEGPANSSKTCWC 212
RMRASNELALAELEEEEGKPEGPANSSKTCWC
Sbjct: 181 RMRASNELALAELEEEEGKPEGPANSSKTCWC 212

Database: /work/eda/blast/public/pataa.fasta
Posted date: May 28, 2003 5:56 PM
Number of letters in database: 19,610,776
Number of sequences in database: 119,338

Lambda	K	H
0.317	0.134	0.389

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 7881817

Number of Sequences: 119338

Number of extensions: 292297

Number of successful extensions: 1272

Number of sequences better than 1.0e-08: 151

Number of HSP's better than 0.0 without gapping: 47

Number of HSP's successfully gapped in prelim test: 104

Number of HSP's that attempted gapping in prelim test: 1052

Number of HSP's gapped (non-prelim): 151

length of query: 212

length of database: 19,610,776

effective HSP length: 50

effective length of query: 162

effective length of database: 13,643,876

effective search space: 2210307912

effective search space used: 2210307912

T: 11

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

S1: 41 (21.7 bits)

S2: 137 (57.8 bits)

PTO/SB/08B (10-01)
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